

#2

OIPE

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/006,366

DATE: 12/17/2001  
TIME: 11:09:46

Input Set : A:\RTS-0332 Sequence Listing.txt  
Output Set: N:\CRF3\12172001\J006366.raw

ENTERED

6 <110> APPLICANT: C. Frank Bennett  
7 Kenneth W. Dobie  
9 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF MHC CLASS II TRANSACTIVATOR  
EXPRESSION  
11 <130> FILE REFERENCE: RTS-0332  
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/006,366  
C--> 13 <141> CURRENT FILING DATE: 2001-11-05  
13 <160> NUMBER OF SEQ ID NOS: 98  
16 <210> SEQ ID NO: 1  
17 <211> LENGTH: 20  
18 <212> TYPE: DNA  
19 <213> ORGANISM: Artificial Sequence  
21 <220> FEATURE:  
23 <223> OTHER INFORMATION: Antisense Oligonucleotide  
25 <400> SEQUENCE: 1  
26 tccgtcatcg ctcctcaggg  
29 <210> SEQ ID NO: 2  
30 <211> LENGTH: 20  
31 <212> TYPE: DNA  
32 <213> ORGANISM: Artificial Sequence  
34 <220> FEATURE:  
36 <223> OTHER INFORMATION: Antisense Oligonucleotide  
38 <400> SEQUENCE: 2  
39 atgcattctg ccccaagga  
42 <210> SEQ ID NO: 3  
43 <211> LENGTH: 6672  
44 <212> TYPE: DNA  
45 <213> ORGANISM: Homo sapiens  
47 <220> FEATURE:  
49 <221> NAME/KEY: CDS  
50 <222> LOCATION: (139)...(3531)  
52 <400> SEQUENCE: 3  
53 cctcccaact ggtgactgg tagtgatgag gctgtgtgt tctgagctgg gcatccgaag 60  
54 gcatccttgg ggaagctgag ggcacgagga ggggctgcca gactccggga gctgctgcct 120  
55 ggctgggatt cctacaca atg cgt tgc ctg gct cca cgc cct gct ggg tcc 171  
56 Met Arg Cys Leu Ala Pro Arg Pro Ala Gly Ser  
57 1 5 10  
59 tac ctg tca gag ccc caa ggc agc tca cag tgt gcc acc atg gag ttg 219  
60 Tyr Leu Ser Glu Pro Gln Gly Ser Ser Gln Cys Ala Thr Met Glu Leu  
61 15 20 25  
63 ggg ccc cta gaa ggt ggc tac ctg gag ctt ctt aac agc gat gct gac 267  
64 Gly Pro Leu Glu Gly Tyr Leu Glu Leu Leu Asn Ser Asp Ala Asp  
65 30 35 40  
67 ccc ctg tgc ctc tac cac ttc tat gac cag atg gac ctg gct gga gaa 315  
68 Pro Leu Cys Leu Tyr His Phe Tyr Asp Gln Met Asp Leu Ala Gly Glu  
69 45 50 55  
71 gaa gag att gag ctc tac tca gaa ccc gac aca gac acc atc aac tgc 363  
72 Glu Glu Ile Glu Leu Tyr Ser Glu Pro Asp Thr Asp Thr Ile Asn Cys

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73	60	65	70	75	411
75	gac cag ttc agc agg ctg ttg gac atg gaa ggt gat gaa gag acc				
76	Asp Gln Phe Ser Arg Leu Leu Cys Asp Met Glu Gly Asp Glu Glu Thr				
77	80	85	90		459
79	agg gag gct tat gcc aat atc gcg gaa ctg gac cag tat gtc ttc cag				
80	Tyr Ala Asn Ile Ala Glu Leu Asp Gln Tyr Val Phe Gln				
81	95	100	105		507
83	gac tcc cag ctg gag ggc ctg agc aag gac att ttc aag cac ata gga				
84	Asp Ser Gln Leu Glu Gly Leu Ser Lys Asp Ile Phe Lys His Ile Gly				
85	110	115	120		555
87	cca gat gaa gta atc ggt gag agt atg gag atg cca gca gaa gtt ggg				
88	Pro Asp Glu Val Ile Gly Glu Ser Met Glu Met Pro Ala Glu Val Gly				
89	125	130	135		603
91	cag aaa agt cag aaa aga ccc ttc cca gag gag ctt ccg gca gac ctg				
92	Gln Lys Ser Gln Lys Arg Pro Phe Pro Glu Glu Leu Pro Ala Asp Leu				
93	140	145	150	155	651
95	aag cac tgg aag cca gct gag ccc ccc act gtc gtc act ggc agt ctc				
96	Lys His Trp Lys Pro Ala Glu Pro Pro Thr Val Val Thr Gly Ser Leu				
97	160	165	170		699
99	cta gtg gga cca gtg agc gac tgc tcc acc ctg ccc tgc ctg cca ctg				
100	Leu Val Gly Pro Val Ser Asp Cys Ser Thr Leu Pro Cys Leu Pro Leu				
101	175	180	185		747
103	cct gcg ctg ttc aac cag gag cca gcc tcc ggc cag atg cgc ctg gag				
104	Pro Ala Leu Phe Asn Gln Glu Pro Ala Ser Gly Gln Met Arg Leu Glu				
105	190	195	200		795
107	aaa acc gac cag att ccc atg ctc ttc tcc agt tcc tgc ttg agc tgc				
108	Lys Thr Asp Gln Ile Pro Met Pro Phe Ser Ser Ser Leu Ser Cys				
109	205	210	215		843
111	ctg aat ctc ctc gag gga ccc atc cag ttt gtc ccc acc atc tcc act				
112	Leu Asn Leu Pro Glu Gly Pro Ile Gln Phe Val Pro Thr Ile Ser Thr				
113	220	225	230	235	891
115	ctg ccc cat ggg ctc tgg caa atc tct gag gct gga aca ggg gtc tcc				
116	Leu Pro His Gly Leu Trp Gln Ile Ser Glu Ala Gly Thr Gly Val Ser				
117	240	245	250		939
119	agt ata ttc atc tac cat ggt gag gtc ccc cag gcc agc caa gta ccc				
120	Ser Ile Phe Ile Tyr His Gly Glu Val Pro Gln Ala Ser Gln Val Pro				
121	255	260	265		987
123	cct ccc agt gga ttc act gtc cac ggc ctc cca aca tct cca gac cgg				
124	Pro Pro Ser Gly Phe Thr Val His Gly Leu Pro Thr Ser Pro Asp Arg				
125	270	275	280		1035
127	cca ggc tcc acc agc ccc ttc gct cca tca gcc act gac ctg ccc agc				
128	Pro Gly Ser Thr Ser Pro Phe Ala Pro Ser Ala Thr Asp Leu Pro Ser				
129	285	290	295		1083
131	atg ctc gaa ctc gcc acc tcc cga gca aac atg aca gag cac aag				
132	Met Pro Glu Pro Ala Leu Thr Ser Arg Ala Asn Met Thr Glu His Lys				
133	300	305	310	315	1131
135	acg tcc ccc acc caa tgc ccg gca gct gga gag gtc tcc aac aag ctt				
136	Thr Ser Pro Thr Gln Cys Pro Ala Ala Gly Glu Val Ser Asn Lys Leu				
137	320	325	330		

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139 cca aaa tgg cct gag ccg gtg gag cag ttc tac cgc tca ctg cag gac	1179
140 Pro Lys Trp Pro Glu Pro Val Glu Gln Phe Tyr Arg Ser Leu Gln Asp	
141 335 340 345	1227
143 acg tat ggt gcc gag ccc gca ggc ccg gat ggc atc cta gtg gag gtg	
144 Thr Tyr Gly Ala Glu Pro Ala Gly Pro Asp Gly Ile Leu Val Glu Val	
145 350 355 360	1275
147 gat ctg gtg cag gcc agg ctg gag agg agc agc aag agc ctg gag	
148 Asp Leu Val Gln Ala Arg Leu Glu Arg Ser Ser Lys Ser Leu Glu	
149 365 370 375	
151 cgg gaa ctg gcc acc ccg gac tgg gca gaa cgg cag ctg gcc caa gga	1323
152 Arg Glu Leu Ala Thr Pro Asp Trp Ala Glu Arg Gln Leu Ala Gln Gly	
153 380 385 390 395	1371
155 ggc ctg gct gag gtg ctg ttg gct gcc aag gag cac cgg cgg cgt	
156 Gly Leu Ala Glu Val Leu Ala Ala Lys Glu His Arg Arg Pro Arg	
157 400 405 410	1419
159 gag aca cga gtg att gct gtg ctg ggc aaa gct ggt cag ggc aag agc	
160 Glu Thr Arg Val Ile Ala Val Leu Gly Lys Ala Gly Gln Gly Lys Ser	
161 415 420 425	1467
163 tat tgg gct ggg gca gtg agc cgg gcc tgg gct tgt ggc cgg ctt ccc	
164 Tyr Trp Ala Gly Ala Val Ser Arg Ala Trp Ala Cys Gly Arg Leu Pro	
165 430 435 440	1515
167 cag tac gac ttt gtc ttc tct gtc ccc tgc cat tgc ttg aac cgt cgg	
168 Gln Tyr Asp Phe Val Phe Ser Val Pro Cys His Cys Leu Asn Arg Pro	
169 445 450 455	1563
171 ggg gat gcc tat ggc ctg cag gat ctg ctc ttc tcc ctg ggc cca cag	
172 Gly Asp Ala Tyr Gly Leu Gln Asp Leu Leu Phe Ser Leu Gly Pro Gln	
173 460 465 470 475	1611
175 cca ctc gtg gcg gcc gat gag gtt ttc agc cac atc ttg aag aga cct	
176 Pro Leu Val Ala Ala Asp Glu Val Phe Ser His Ile Leu Lys Arg Pro	
177 480 485 490	1659
179 gac cgc gtt ctg ctc atc cta gac gcc ttc gag gag ctg gaa ggc caa	
180 Asp Arg Val Leu Leu Ile Leu Asp Ala Phe Glu Leu Glu Ala Gln	
181 495 500 505	1707
183 gat ggc ttc ctg cac agc acg tgc gga cgg gca ccc gcg gag ccc tgc	
184 Asp Gly Phe Leu His Ser Thr Cys Gly Pro Ala Pro Glu Pro Cys	
185 510 515 520	1755
187 tcc ctc cgg ggg ctg gtc gcc ggc ctt ttc cag aag aag ctg ctc cga	
188 Ser Leu Arg Gly Leu Leu Ala Gly Leu Phe Gln Lys Lys Leu Leu Arg	
189 525 530 535	1803
191 ggt tgc acc ctc ctc aca gcc cgg ccc cgg ggc cgc ctg gtc cag	
192 Gly Cys Thr Leu Leu Leu Thr Ala Arg Pro Arg Gly Arg Leu Val Gln	
193 540 545 550 555	1851
195 agc ctg agc aag gcc gac gcc cta ttt gag ctg tcc ggc ttc tcc atg	
196 Ser Leu Ser Lys Ala Asp Ala Leu Phe Glu Leu Ser Gly Phe Ser Met	
197 560 565 570	1899
199 gag cag gcc cag gca tac gtg atg cgc tac ttt gag agc tca ggg atg	
200 Glu Gln Ala Gln Ala Tyr Val Met Arg Tyr Phe Glu Ser Ser Gly Met	
201 575 580 585	1947
203 aca gag cac caa gac aga gcc ctg acg ctc ctc cgg gac cgg cca ctt	

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204	Thr	Glu	His	Gln	Asp	Arg	Ala	Leu	Thr	Leu	Leu	Arg	Asp	Arg	Pro	Leu
205																600
	590															1995
207	ctt	ctc	agt	cac	agc	cac	agc	cct	act	ttg	tgc	cgg	gca	gtg	tgc	cag
208	Leu	Leu	Ser	His	Ser	His	Ser	Pro	Thr	Leu	Cys	Arg	Ala	Val	Cys	Gln
209																615
	605															2043
211	ctc	tca	gag	gcc	ctg	ctg	gag	ctt	ggg	gag	gac	gcc	aag	ctg	ccc	tcc
212	Leu	Ser	Glu	Ala	Leu	Leu	Glu	Gly	Glu	Asp	Ala	Lys	Leu	Pro	Ser	
213																635
	620															2091
215	acg	ctc	acg	gga	ctc	tat	gtc	ggc	ctg	ggc	cgt	gca	gcc	ctc	gac	
216	Thr	Leu	Thr	Gly	Leu	Tyr	Val	Gly	Leu	Leu	Gly	Arg	Ala	Ala	Leu	Asp
217																650
	640															2139
219	agc	ccc	ccc	ggg	gcc	ctg	gca	gag	ctg	gcc	aag	ctg	gcc	tgg	gag	ctg
220	Ser	Pro	Pro	Gly	Ala	Leu	Ala	Glu	Leu	Ala	Lys	Leu	Ala	Trp	Glu	Leu
221																665
	655															2187
223	ggc	cgc	aga	cat	caa	agt	acc	cta	cag	gag	gac	cag	ttc	cca	tcc	gca
224	Gly	Arg	Arg	His	Gln	Ser	Thr	Leu	Gln	Glu	Asp	Gln	Phe	Pro	Ser	Ala
225																680
	670															2235
227	gac	gtg	agg	acc	tgg	gcg	atg	gcc	aaa	gcc	tta	gtc	caa	cac	cca	ccg
228	Asp	Val	Arg	Thr	Trp	Ala	Met	Ala	Lys	Gly	Leu	Val	Gln	His	Pro	Pro
229																695
	685															2283
231	cg	gcc	gca	gag	tcc	gag	ctg	gcc	ttc	ccc	agc	ttc	ctc	ctg	caa	tgc
232	Arg	Ala	Ala	Glu	Ser	Glu	Leu	Ala	Phe	Pro	Ser	Phe	Leu	Gln	Cys	
233																715
	700															2331
235	tcc	ctg	ggg	gcc	ctg	tgg	ctg	gct	ctg	agt	ggc	gaa	atc	aag	gac	aag
236	Phe	Leu	Gly	Ala	Leu	Trp	Leu	Ala	Leu	Ser	Gly	Glu	Ile	Lys	Asp	Lys
237																730
	720															2379
239	gag	ctc	ccg	cag	tac	cta	gca	ttg	acc	cca	agg	aag	aag	agg	ccc	tat
240	Glu	Leu	Pro	Gln	Tyr	Leu	Ala	Leu	Thr	Pro	Arg	Lys	Lys	Arg	Pro	Tyr
241																745
	735															2427
243	gac	aac	tgg	ctg	gag	gcc	gtg	cca	cgc	ttt	ctg	gct	ggg	ctg	atc	tcc
244	Asp	Asn	Trp	Leu	Glu	Gly	Val	Pro	Arg	Phe	Leu	Ala	Gly	Leu	Ile	Phe
245																755
	750															2475
247	cag	cct	ccc	gcc	cgc	tgc	ctg	gga	gcc	cta	ctc	ggg	cca	tcg	gcg	gct
248	Gln	Pro	Pro	Ala	Arg	Cys	Leu	Gly	Ala	Leu	Leu	Gly	Pro	Ser	Ala	Ala
249																775
	765															2523
251	gcc	tgc	gtg	gac	agg	aag	cag	aag	gtg	ctt	gct	agg	tac	ctg	aag	ccg
252	Ala	Ser	Val	Asp	Arg	Lys	Gln	Lys	Val	Leu	Ala	Arg	Tyr	Leu	Lys	
253																795
	780															2571
255	ctg	cag	ccg	ggg	aca	ctg	ccg	gcc	cgg	cag	ctg	ctt	gag	ctg	ctg	cac
256	Leu	Gln	Pro	Gly	Thr	Leu	Arg	Ala	Arg	Gln	Leu	Leu	Glu	Leu	Leu	His
257																805
	800															810
259	tgc	gcc	cac	gag	gcc	gag	gag	gct	gga	att	tgg	cag	cac	gtg	gta	cag
260	Cys	Ala	His	Glu	Ala	Glu	Glu	Ala	Gly	Ile	Trp	Gln	His	Val	Val	Gln
261																820
	815															825
263	gag	ctc	ccc	ggc	cgc	ctc	tct	ttt	ctg	ggc	acc	cgc	ctc	acg	cct	cct
264	Glu	Leu	Pro	Gly	Arg	Leu	Ser	Phe	Leu	Gly	Thr	Arg	Leu	Thr	Pro	Pro
265																835
	830															840
267	gat	gca	cat	gta	ctg	ggc	aag	gcc	ttg	gag	gct	gct	ggc	caa	gac	ttc
268	Asp	Ala	His	Val	Leu	Gly	Lys	Ala	Leu	Glu	Ala	Ala	Gly	Gln	Asp	Phe

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269	845	850	855	2763
271	tcc ctg gac ctc cgc agc act ggc att tgc ccc tct gga ttg ggg agc			
272	Ser Leu Asp Leu Arg Ser Thr Gly Ile Cys Pro Ser Gly Leu Gly Ser			
273	860	865	870	875
275	ctc gtg gga ctc agc tgt gtc acc cgt ttc agg gct gcc ttg agc gac			2811
276	Leu Val Gly Leu Ser Cys Val Thr Arg Phe Arg Ala Ala Leu Ser Asp			
277	880	885	890	2859
279	acg gtg gcg ctg tgg gag tcc ctg cgg cag cat ggg gag acc aag cta			
280	Thr Val Ala Leu Trp Glu Ser Leu Arg Gln His Gly Glu Thr Lys Leu			
281	895	900	905	2907
283	ctt cag gca gca gag gag aag ttc acc atc gag cct ttc aaa gcc aag			
284	Leu Gln Ala Ala Glu Glu Lys Phe Thr Ile Glu Pro Phe Lys Ala Lys			
285	910	915	920	2955
287	tcc ctg aag gat gtg gaa gac ctg gga aag ctt gtg cag act cag agg			
288	Ser Leu Lys Asp Val Glu Asp Leu Gly Lys Leu Val Gln Thr Gln Arg			
289	925	930	935	3003
291	acg aga agt tcc tcg gaa gac aca gct ggg gag ctc cct gct gtt cgg			
292	Thr Arg Ser Ser Glu Asp Thr Ala Gly Glu Leu Pro Ala Val Arg			
293	940	945	950	3051
295	gac cta aag aaa ctg gag ttt gcg ctg ggc cct gtc tca ggc ccc cag			
296	Asp Leu Lys Lys Leu Glu Phe Ala Leu Gly Pro Val Ser Gly Pro Gln			
297	960	965	970	3099
299	gct ttc ccc aaa ctg gtg cgg atc ctc acg gcc ttt tcc tcc ctg cag			
300	Ala Phe Pro Lys Leu Val Arg Ile Leu Thr Ala Phe Ser Ser Leu Gln			
301	975	980	985	3147
303	cat ctg gac ctg gat gcg ctg agt gag aac aag atc ggg gac gag ggt			
304	His Leu Asp Leu Asp Ala Leu Ser Glu Asn Lys Ile Gly Asp Glu Gly			
305	990	995	1000	3195
307	gtc tcg cag ctc tca gcc acc ttc ccc cag ctg aag tcc ttg gaa acc			
308	Val Ser Gln Leu Ser Ala Thr Phe Pro Gln Leu Lys Ser Leu Glu Thr			
309	1005	1010	1015	3243
311	ctc aat ctg tcc cag aac aac atc act gac ctg ggt gcc tac aaa ctc			
312	Leu Asn Leu Ser Gln Asn Asn Ile Thr Asp Leu Gly Ala Tyr Lys Leu			
313	1020	1025	1030	1035
315	gcc gag gcc ctg cct tcg ctc gct gca tcc ctg ctc agg cta agc ttg			3291
316	Ala Glu Ala Leu Pro Ser Leu Ala Ala Ser Leu Leu Arg Leu Ser Leu			
317	1040	1045	1050	3339
319	tac aat aac tgc atc tgc gac gtg gga gcc gag agc ttg gct cgt gtg			
320	Tyr Asn Asn Cys Ile Cys Asp Val Gly Ala Glu Ser Leu Ala Arg Val			
321	1055	1060	1065	3387
323	ctt ccg gac atg gtg tcc ctc ccg gtg atg gac gtc cag tac aac aag			
324	Leu Pro Asp Met Val Ser Leu Arg Val Met Asp Val Gln Tyr Asn Lys			
325	1070	1075	1080	3435
327	ttc acg gct gcc ggg gcc cag cag ctc gct gcc agc ctt ccg agg tgt			
328	Phe Thr Ala Ala Gly Ala Gln Gln Leu Ala Ala Ser Leu Arg Arg Cys			
329	1085	1090	1095	3483
331	cct cat gtg gag acg ctg gcg atg tgg acg ccc acc atc cca ttc agt			
332	Pro His Val Glu Thr Ile Ala Met Trp Thr Pro Thr Ile Pro Phe Ser			
333	1105	1110	1115	

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/006,366

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Input Set : A:\RTS-0332 Sequence Listing.txt  
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L:13 M:270 C: Current Application Number differs, Replaced Current Application No  
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:580 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:14